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Supplementary Information

**Production of polyhydroxyalkanoates using a novel,
metagenomics identified, class III synthase.**

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Table S1: Primers used for metagenomics DNA amplification and PCR cloning confirmation

Primer	Sequence	Length (bp)	Tm (°C)
AUR_1116_Fw	CTAGTGAATGAAGAGACCGCCGTTG	25	64.0
AUR_1116_Rev	CGCATCAGACCGAGCGCTC	19	65.7
AUR_19_Fw	CTAGTGAATGAAGAGACCGCCG	22	62.3
AUR_19_Rev	ATTGACCAGAGCGAAGGCCG	20	65.2
AUR_5970_Fw	TCAGTGCATGAAGAGACCGCCGTTT	25	67.6
AUR_5970_Rev	TAACCGCGGCAGTCCGTG	18	65.6
CYC_302_Fw	TCAGGAGCGTTCGTTTCAGCCAC	22	66.6
CYC_302_Rev	GGTAATTCACCACGCGCCCCG	20	66.6
1116_cpcr_Fw	TGTCTATCTCATCGACTGGG	20	58.5
1116_cpcr_Rev	AAGATCCATTTCTCCATGCG	20	57.2
5970_cpcr_Fw	GTCAAGGACAATCTGAACCG	20	58.7
5970_cpcr_Rev	GATTCAATGGACCTGATGGC	20	58.8
5970_cpcr_phaP_Fw	TTAGGCGGCCGGAACAGC	18	66
5970_cpcr_phaP_Rev	ATGACGACCAACGACACCCTG	25	65
302_cpcr_Fw	GAAGTCCTTGATGAACTGGC	20	58.5
302_cpcr_Rev	GTCTATCTCATCGACTGGGG	20	60.1

Table S2: PHA synthase search using KOFamScan.

Name	KO	Threshold	Ccore	E-value	KO definition
AUR_19_83	K22881	56.1	231.6	1.00E-70	poly[(R)-3-hydroxyalkanoate] polymerase subunit PhaE
AUR_19_84	K03821	181.9	340.4	1.50E-103	poly[(R)-3-hydroxyalkanoate] polymerase subunit PhaC [EC:2.3.1.304]
AUR_5970_5	K22881	56.1	240.4	2.30E-73	poly[(R)-3-hydroxyalkanoate] polymerase subunit PhaE
AUR_5970_6	K03821	181.9	340.5	1.30E-103	poly[(R)-3-hydroxyalkanoate] polymerase subunit PhaC [EC:2.3.1.304]

CYC_302_30	K03821	181.9	341.5	6.80E-104	poly[(R)-3-hydroxyalkanoate] polymerase subunit PhaC [EC:2.3.1.304]
CYC_302_31	K22881	56.1	238.3	9.90E-73	poly[(R)-3-hydroxyalkanoate] polymerase subunit PhaE
CYC_1116_15	K22881	56.1	231.6	1.00E-70	poly[(R)-3-hydroxyalkanoate] polymerase subunit PhaE
CYC_1116_16	K03821	181.9	340.4	1.50E-103	poly[(R)-3-hydroxyalkanoate] polymerase subunit PhaC [EC:2.3.1.304]

Table S3: PHA synthesis cluster annotation using BLAST, against the nr database

Gene ID	Length (aa)	Annotation	Best hit lineage	Identity percentage	GenBank
AUR_19_phaB	247	acetoacetyl-CoA reductase	<i>Thiocapsa imhoffii</i>	90.65	NCA70382.1
AUR_19_phaP	122	phasin family protein	<i>Thiocapsa imhoffii</i>	77.69	NCA70383.1
AUR_19_phaR	175	polyhydroxyalkanoate synthesis repressor PhaR	<i>Thiocapsa sp.</i>	80.24	NCA70385.1
AUR_19_phaA	395	acetyl-CoA C-acetyltransferase	<i>Thiocapsa sp.</i> KS1	90.36	NCA70385.1
AUR_19_phaE	351	poly[(R)-3-hydroxyalkanoate] polymerase subunit PhaE [K22881]	<i>Thiocapsa sp.</i>	72.07	NCA70386.1
AUR_19_phaC	357	poly[(R)-3-hydroxyalkanoate] polymerase subunit PhaC [K03821]	<i>Thiocapsa sp.</i>	93.54	NCA70387.1
AUR_5970_phaB	247	acetoacetyl-CoA reductase	<i>Thiocapsa sp.</i> UBA6158	99.19	NCC28072.1
AUR_5970_phaP	122	phasin family protein	<i>Thiocapsa sp.</i> UBA6158	97.52	NCC28073.1
AUR_5970_phaR	176	polyhydroxyalkanoate synthesis repressor PhaR	<i>Thiocapsa sp.</i> UBA6158	99.42	NCC28074.1
AUR_5970_phaA	395	acetyl-CoA C-acetyltransferase	<i>Thiocapsa marina</i>	98.98	NCC28075.1
AUR_5970_phaE	357	poly[(R)-3-hydroxyalkanoate] polymerase subunit PhaE [K22881]	<i>Thiocapsa sp.</i> UBA6158	97.19	NCC28076.1
AUR_5970_phaC	357	poly[(R)-3-hydroxyalkanoate] polymerase subunit PhaC [K03821]	<i>Thiocapsa sp.</i> UBA6158	99.44	NCC28077.1
CYC_302_phaC	357	poly[(R)-3-hydroxyalkanoate] polymerase subunit PhaC [K03821]	<i>Chromatiaceae bacterium</i>	96.06	NCA87864.1
CYC_302_phaE	355	poly[(R)-3-hydroxyalkanoate] polymerase subunit PhaE [K22881]	<i>Chromatiaceae bacterium</i>	92.86	NCA87865.1
CYC_302_phaA	395	acetyl-CoA C-acetyltransferase	<i>Chromatiaceae bacterium</i>	97.96	NCA87866.1
CYC_302_phaR	154	polyhydroxyalkanoate synthesis repressor PhaR	<i>Chromatiaceae bacterium</i>	94.12	NCA87867.1

CYC_302_phaP	123	phasin family protein	<i>Candidatus Thioaporhodococcus sediminis</i>	95.08	NCA87868.1
CYC_302_phaB	250	acetoacetyl-CoA reductase	<i>Chromatiaceae bacterium</i>	97.55	NCA87869.1
CYC_1116_phaB	247	acetoacetyl-CoA reductase	<i>Thiocapsa imhoffii</i>	90.65	NCA70382.1
CYC_1116_phaP	122	phasin family protein	<i>Thiocapsa imhoffii</i>	77.69	NCA70383.1
CYC_1116_phaR	175	polyhydroxyalkanoate synthesis repressor PhaR	<i>Thiocapsa sp.</i>	80.24	NCA70384.1
CYC_1116_phaA	395	acetyl-CoA C-acetyltransferase	<i>Thiocapsa sp. KS1</i>	90.36	NCA70385.1
CYC_1116_phaE	351	poly[(R)-3-hydroxyalkanoate] polymerase subunit PhaE [K22881]	<i>Thiocapsa sp.</i>	72.07	NCA70386.1
CYC_1116_phaC	357	poly[(R)-3-hydroxyalkanoate] polymerase subunit PhaC [K03821]	<i>Gammaproteobacteria bacterium</i>	93.54	NCA70387.1